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401  GGCTCTCATG GCTTCTCTCT ATGTCCACAT GTTCCTCATG GCCAGACTCC
451  ACATTAAGAG GATCGCCGTC CTCCCAGGCA CTGGCACCAT CCGCCAAGGT
501  GCCAACATGA AGGGGGCAAT TACCCTGACC ATCTTGATTG GGGTCTTTGT
551  GGTCTGCTGG GCCCCCTTCT TCCTCCACTT AATATTCTAT ATCTCCTGCC
```

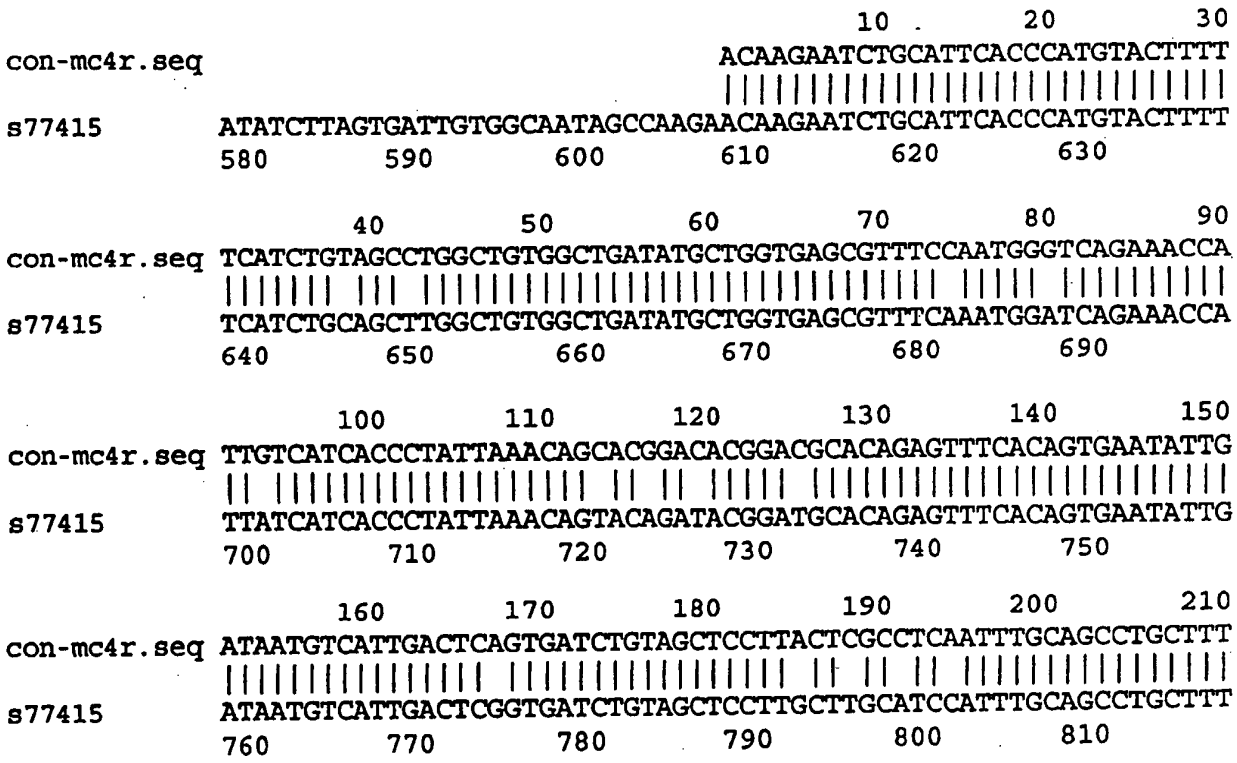
Fig. 1

601 CCCAGAATCC ATACTGTGTG TGCTTCATGT CTCACTTTAA TTTGTATCTC

651 ATCCTGATCA TGTGTAATTC CATCATCXAT CCCCTGATTT ATGCACTCCG

701 GAGCCAAGAA CTGAGGAAAA CCTTCAAAGA GATCATCTGT TGCTAT

Fig. 1A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40 50 60 70 80 90
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100 110 120 130 140 150
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Fig.2A

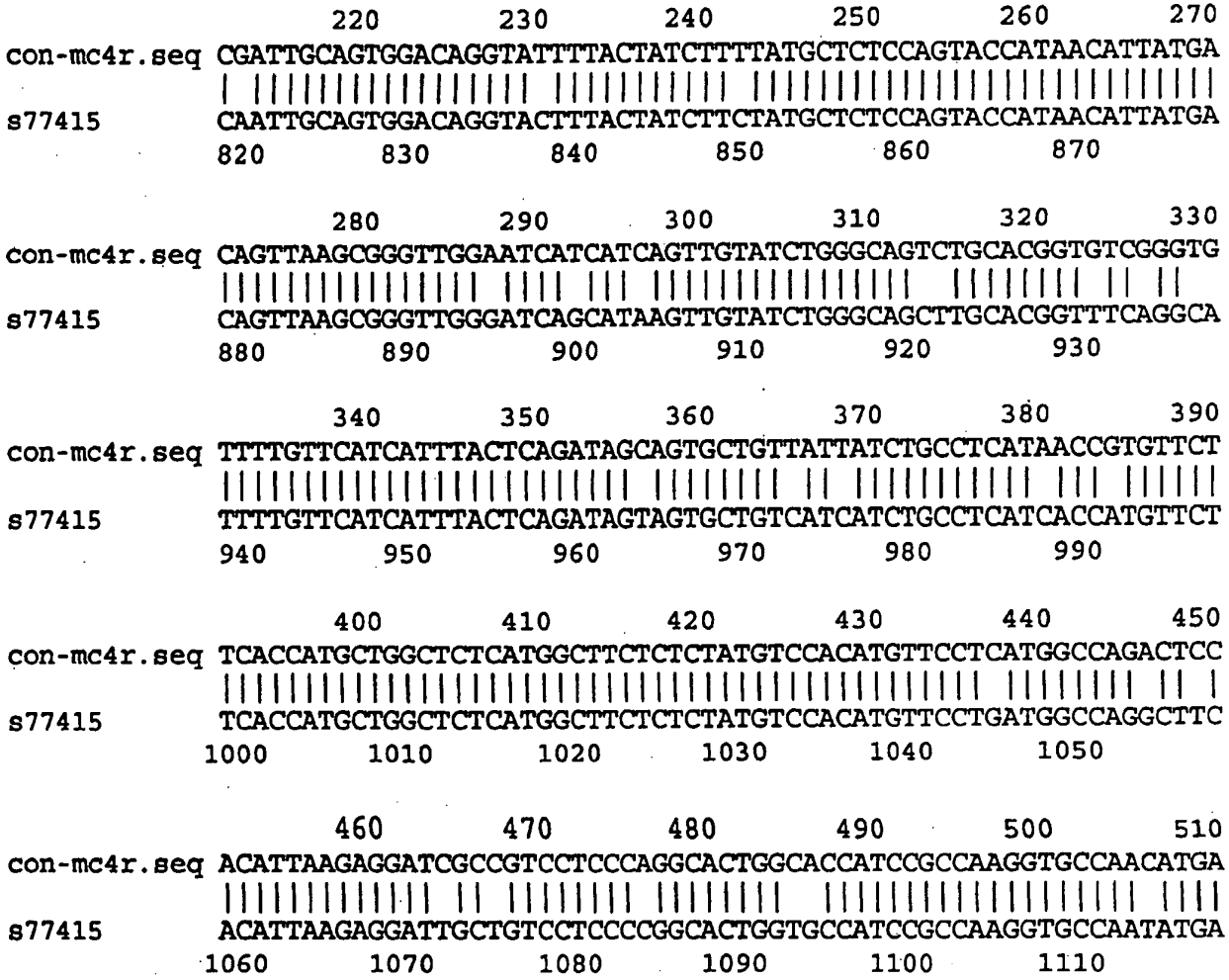
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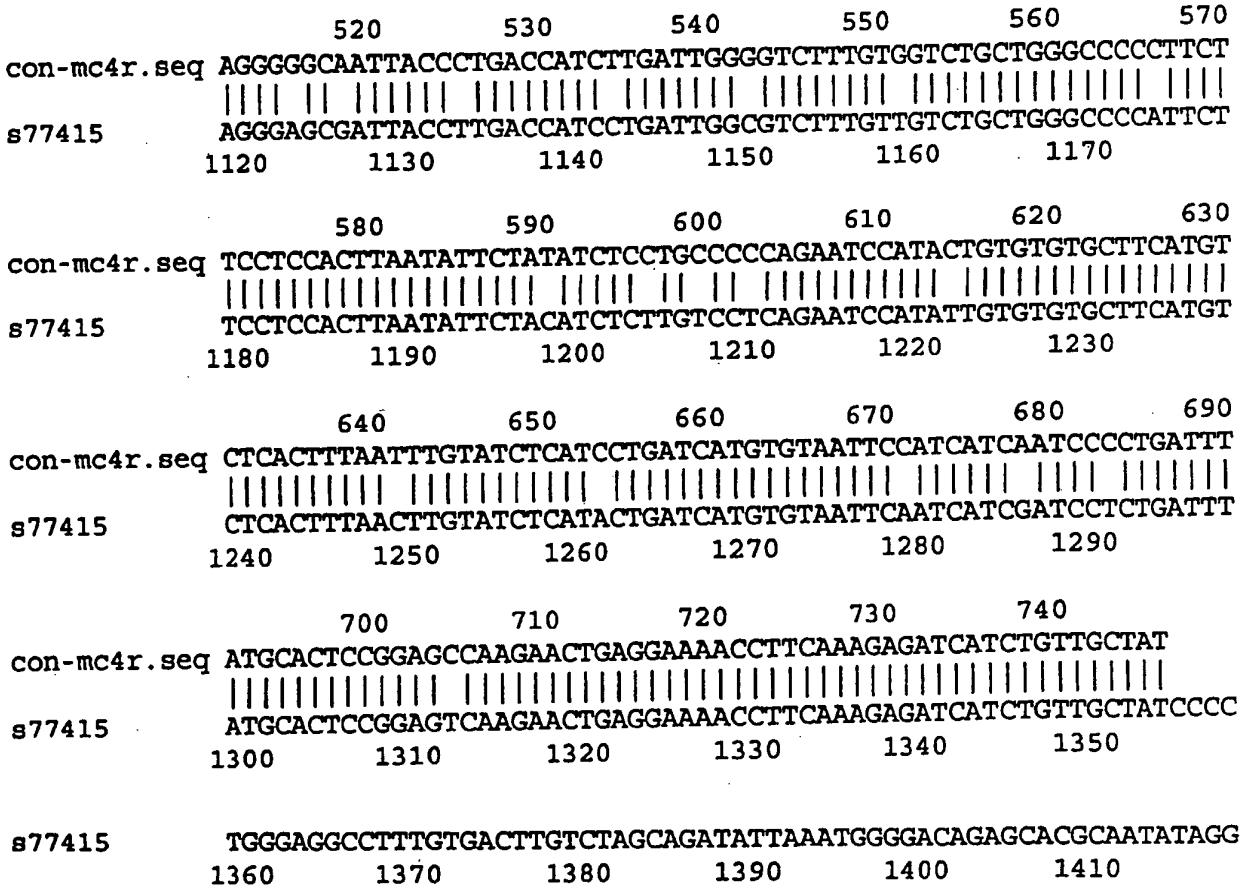
Fig.2B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1360 1370 1380 1390 1400 1410

Fig.2C

```
                    50         60         70         80         90         100
human.pep     QLFVSPEVFVTLGVISLLENILVIVAIAKNKNLHSPMYFFICSLAVADMLVSVSNGSETI
                                                    ||||||||||||||||||||||||||||
mc4r-allel                                          KNLHSPMYFFICSLAVADMLVSVSNGSETI
                                                              10         20         30

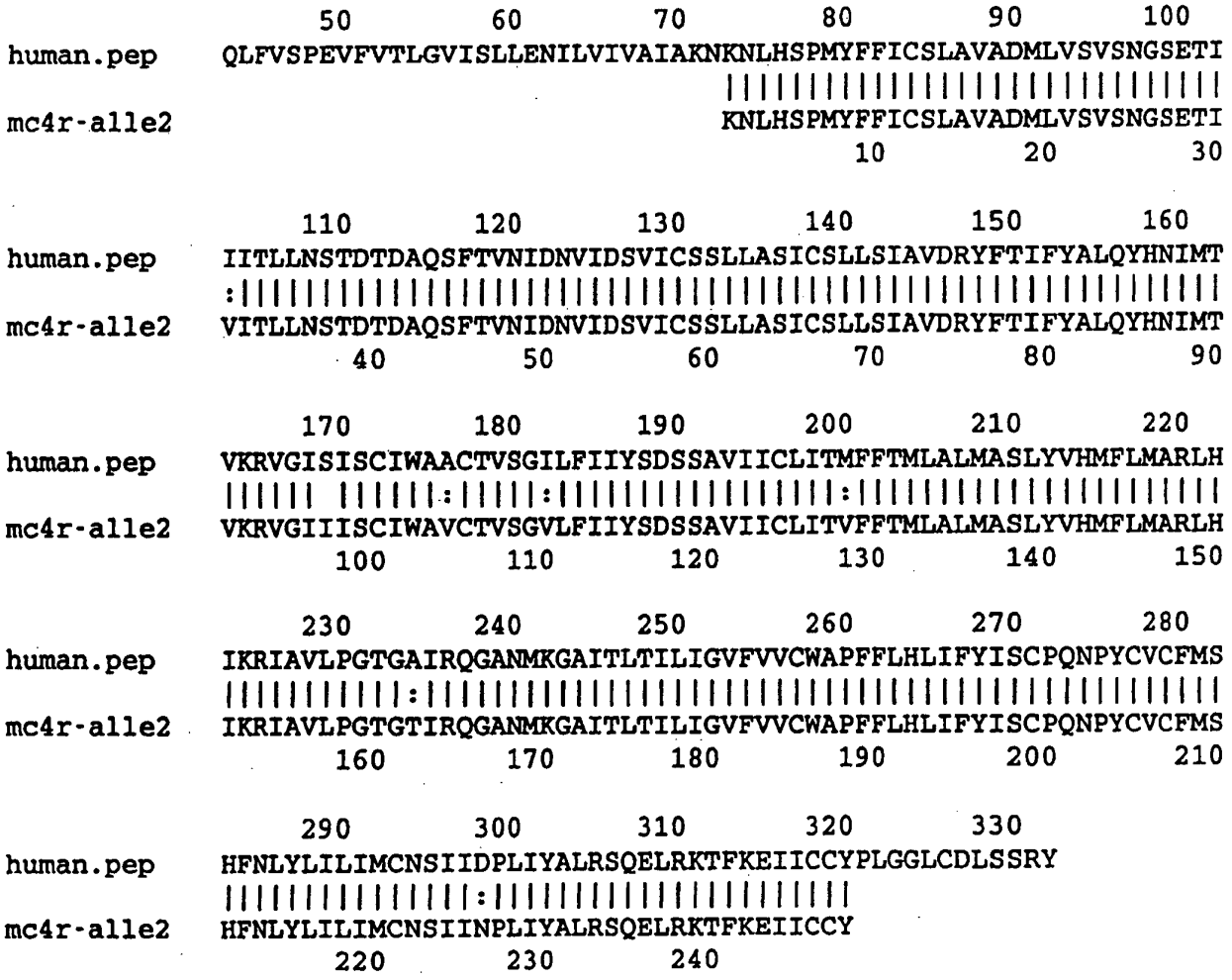
                   110        120        130        140        150        160
human.pep     IITLLNSTDTDAQSFTVNIDNVIDSVICSSLLASICSLLSIAVDRYFTIFYALQYHNIMT
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
mc4r-allel    VITLLNSTDTDAQSFTVNIDNVIDSVICSSLLASICSLLSIAVDRYFTIFYALQYHNIMT
                       40         50         60         70         80         90

                   170        180        190        200        210        220
human.pep     VKRVGISISCIWAACTVSGILFIIYSDSSAVIICLITMFFTMLALMASLYVHMFLMARLH
              |||||| ||||||:|||||:||||||||||||||:||||||||||||||||||||||||
mc4r-allel    VKRVGIIISCIWAVCTVSGVLFIIYSDSSAVIICLITVFFTMLALMASLYVHMFLMARLH
                      100        110        120        130        140        150

                   230        240        250        260        270        280
human.pep     IKRIAVLPGTGAIRQGANMKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMS
              ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
mc4r-allel    IKRIAVLPGTGTIRQGANMKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMS
                      160        170        180        190        200        210

                   290        300        310        320        330
human.pep     HFNLYLILIMCNSIIDPLIYALRSQELRKTFKEIICCYPLGGLCDLSSRY
              ||||||||||||||||||||||||||||||||||||
mc4r-allel    HFNLYLILIMCNSIIDPLIYALRSQELRKTFKEIICCY
                      220        230        240
```

Fig. 3A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mc4r-alle2 KNLHSPMYFFICSLAVADMLVSVSNGSETI
10 20 30
110 120 130 140 150 160
human.pep IITLLNSTDTDAQSFTVNIDNVIDSVICSSLLASICSLLSIAVDRYFTIFYALQYHNIMT
mc4r-alle2 VITLLNSTDTDAQSFTVNIDNVIDSVICSSLLASICSLLSIAVDRYFTIFYALQYHNIMT
40 50 60 70 80 90
170 180 190 200 210 220
human.pep VKRVGISISCIWAACTVSGILFIIYSDSSAVIICLITMFFTMLALMASLYVHMFLMARLH
mc4r-alle2 VKRVGIIISCIWAVCTVSGVLFIIYSDSSAVIICLITVFFTMLALMASLYVHMFLMARLH
100 110 120 130 140 150
230 240 250 260 270 280
human.pep IKRIAVLPGTGAIRQGANMKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMS
mc4r-alle2 IKRIAVLPGTGTIRQGANMKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMS
160 170 180 190 200 210
290 300 310 320 330
human.pep HFNLYLILIMCNSIIDPLIYALRSQELRKTFKEIICCYPLGGLCDLSSRY
mc4r-alle2 HFNLYLILIMCNSIINPLIYALRSQELRKTFKEIICCY
220 230 240

Fig. 3B

S0082 MC4R rec. fracs.= 0.05, lods = 14.74

CGA MC4R rec. fracs.= 0.14, lods = 6.88

S0020 MC4R rec. fracs.= 0.18, lods = 5.32

S0079 MC4R rec. fracs.= 0.12, lods = 10.35

S0155 MC4R rec. fracs.= 0.14, lods = 7.68

S0122 MC4R rec. fracs.= 0.18, lods = 5.17

S0313 MC4R rec. fracs.= 0.00, lods = 17.76

S0312 MC4R rec. fracs.= 0.20, lods = 5.60

S0311 MC4R rec. fracs.= 0.17, lods = 7.18

S0416 MC4R rec. fracs.= 0.20, lods = 3.21

S0331 MC4R rec. fracs.= 0.02, lods = 21.91

S0396 MC4R rec. fracs.= 0.16, lods = 7.85

BHT0433 MC4R rec. fracs.= 0.02, lods = 21.32

S0536 MC4R rec. fracs.= 0.03, lods = 15.61

CAPN3 MC4R rec. fracs.= 0.12, lods = 6.65

Fig. 4A

```
KGF     MC4R  rec. fracs.=    0.09,    lods =    6.46
MEF2A   MC4R  rec. fracs.=    0.05,    lods =   14.36
MC4R    MC4R  rec. fracs.=    0.00,    lods =   26.19
S0082   MC4R  rec. fracs.=    0.00   0.09,   lods =   15.86
CGA     MC4R  rec. fracs.=    0.07   0.22,   lods =    7.46
S0020   MC4R  rec. fracs.=    0.00   0.25,   lods =    6.33
S0079   MC4R  rec. fracs.=    0.00   0.19,   lods =   11.48
S0155   MC4R  rec. fracs.=    0.00   0.24,   lods =    9.98
S0122   MC4R  rec. fracs.=    0.00   0.27,   lods =    7.10
S0313   MC4R  rec. fracs.=    0.00   0.00,   lods =   17.76
S0312   MC4R  rec. fracs.=    0.04   0.29,   lods =    7.45
```

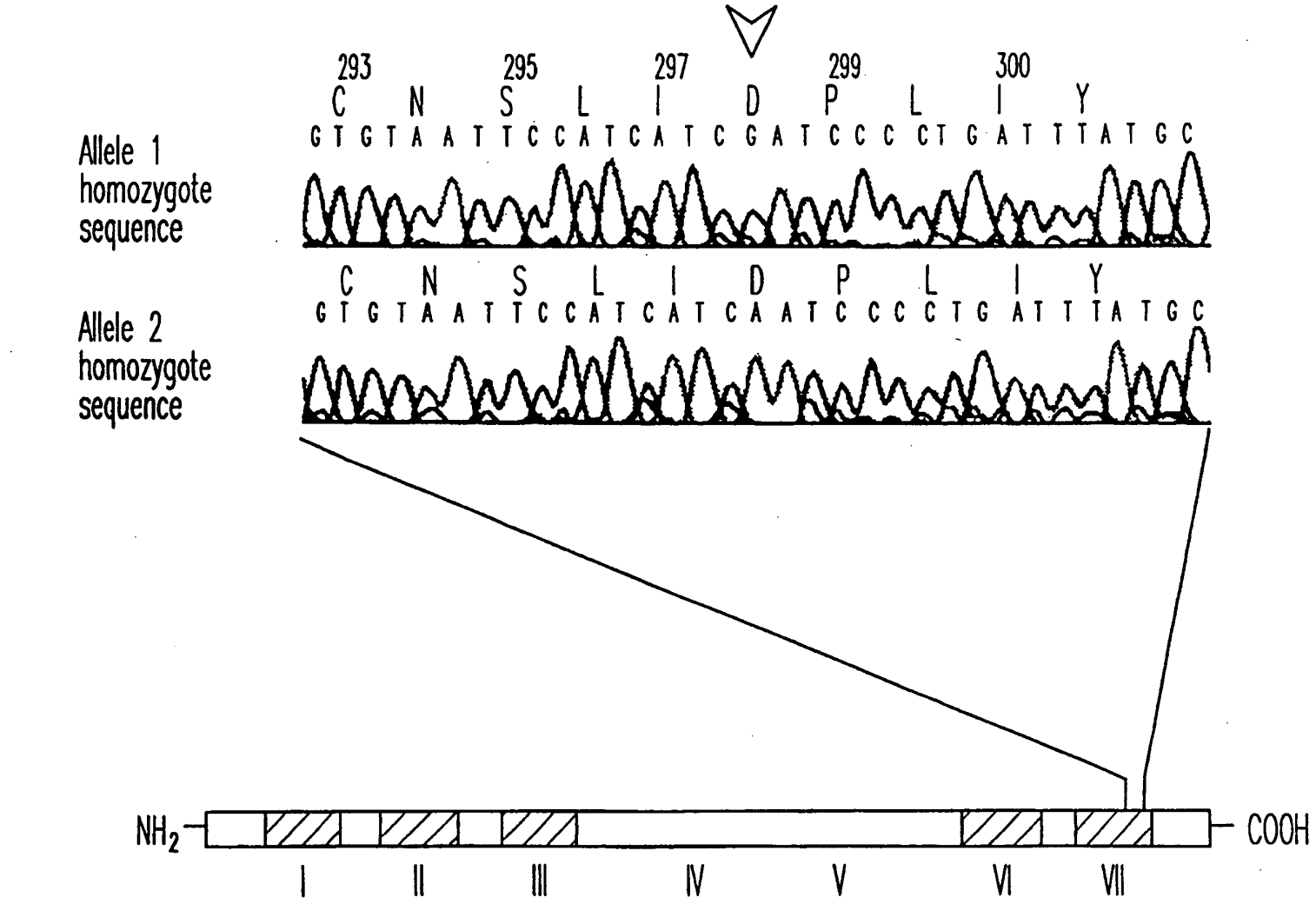
Fig. 4B

```
S0311    MC4R  rec. fracs.=   0.00   0.28,   lods =   9.02
S0416    MC4R  rec. fracs.=   0.00   0.31,   lods =   4.17
S0331    MC4R  rec. fracs.=   0.05   0.00,   lods =  22.14
S0396    MC4R  rec. fracs.=   0.03   0.24,   lods =   9.33
BHT0385  MC4R  rec. fracs.=   0.14   0.36,   lods =   3.46
BHT0433  MC4R  rec. fracs.=   0.05   0.00,   lods =  21.82
S0536    MC4R  rec. fracs.=   0.00   0.05,   lods =  15.77
CAPN3    MC4R  rec. fracs.=   0.00   0.18,   lods =   7.35
KGF      MC4R  rec. fracs.=   0.00   0.17,   lods =   6.74
MEF2A    MC4R  rec. fracs.=   0.10   0.00,   lods =  14.52
MC4R     MC4R  rec. fracs.=   0.00   0.00,   lods =  26.19
```

Fig. 4C

0	ESR			0.0
		0.18	18.4	
1	S0008			18.4
		0.12	11.9	
7	CGA			30.3
		0.03	2.8	
3	S0312			33.1
		0.05	4.9	
4	S0122			38.1
		0.09	9.4	
8	KGF			47.4
		0.06	5.8	
6	CAPN3			53.2
		0.02	2.5	
9	MEF2A			55.7
		0.06	6.1	
5	MC4R			61.8
		0.06	5.6	
10	S0313			67.4
		0.00	0.0	
11	S0082			67.4
		0.03	3.4	
12	S0079			70.8
		0.03	2.5	
14	S0142			73.3
		0.01	1.0	
13	S0020			74.4
		0.04	4.3	
15	S0311			78.7
		0.00	0.0	
16	S0155			78.7
		0.12	12.2	
17	S0113			90.9
		0.20	21.0	
18	S0302			111.9
		0.22	23.4	
19	S0112			135.3

Fig. 4D


293
295
297
299
300
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G T G T A A T T C C A T C A T C A T C G A T C C C C T G A T T T A T G C
Allele 1 homozygote sequence
C N S L I D P L I Y
G T G T A A T T C C A T C A T C A A T C C C C T G A T T T A T G C
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NH2
COOH
I
II
III
IV
V
VI
VII
= Transmembrane domains

Fig. 5

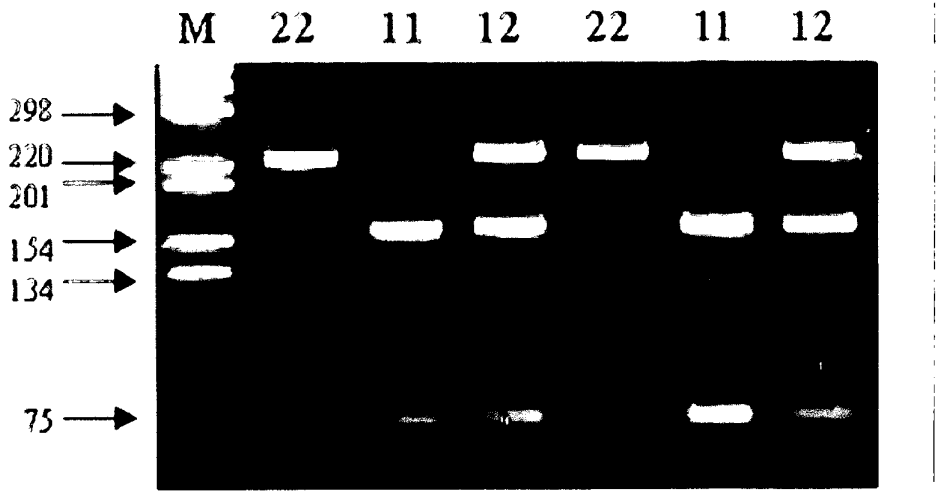
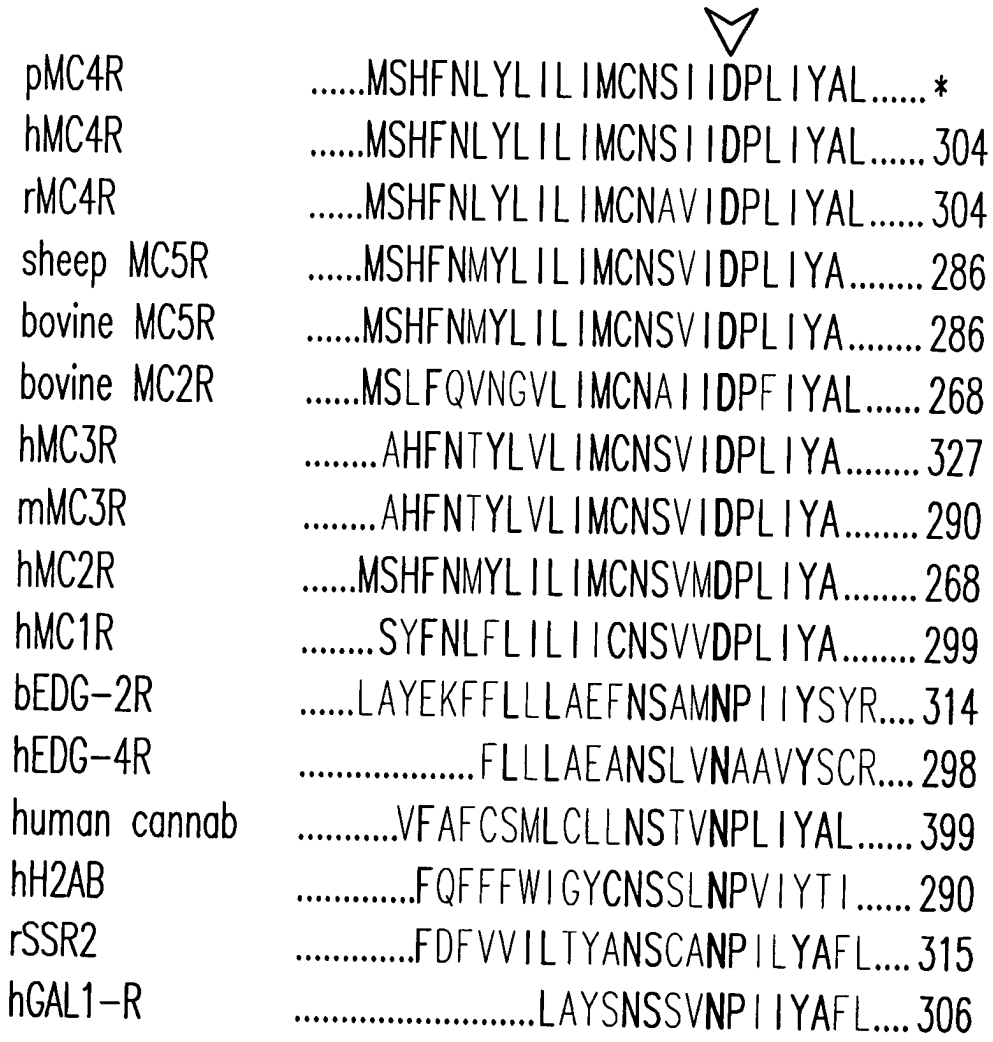


Fig. 6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sheep MC5R .....MSHFNMYLILIMCNSVIDPLIYA..... 286
bovine MC5R .....MSHFNMYLILIMCNSVIDPLIYA..... 286
bovine MC2R .....MSLFQVNGVLIMCNAIIDPFIYAL..... 268
hMC3R .....AHFNTYLVLIMCNSVIDPLIYA..... 327
mMC3R .....AHFNTYLVLIMCNSVIDPLIYA..... 290
hMC2R .....MSHFNMYLILIMCNSVMDPLIYA..... 268
hMC1R .....SYFNLFLILIICNSVVDPLIYA..... 299
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hEDG-4R .....FLLLAEANSLVNAAVYSCR.... 298
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hH2AB .....FQFFFWIGYCNSSLNPVIYTI..... 290
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Fig. 7